ABSTRACT

A computational method system, and computer program are provided for inferring functional links from genome sequences. One method is based on the observation that some pairs of proteins A' and B' have homologs in another organism fused into a single protein chain AB. A trans-genome comparison of sequences can reveal these AB sequences, which are Rosetta Stone sequences because they decipher an interaction between A' and B. Another method compares the genomic sequence of two or more organisms to create a phylogenetic profile for each protein indicating its presence or absence across all the genomes. The profile provides information regarding functional links between different families of proteins. In yet another method a combination of the above two methods is used to predict functional links.

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